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B0132709 Regulator
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AR20585 Sequence
B0132698 Regulator
AR209001 Sequence
B0132699 Regulator
AR482070 Sequence
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B0132700 Regulator
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AR482071 Sequence
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1 (Dasss 1 to 661)
Fischhoff, D.A., Fuchs, R.L., McPherson, S.A., Lavrik, P.B. and
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Pred. No. 2.5e-163;
0; Mismatches 30; Indels
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Insect-resistant plants
Patent: EP 0289479-A2 34 02-NOV-1988;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 34 from Patent EP 0289479.
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BD008400 Glyphosat
AR143713 Sequence
BD008404 Glyphosat
AR143712 Sequence
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AR03011 Sequence
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107318 Sequence 30
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(without alignments)
4649.073 Million cell updates/sec
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Compugen Ltd.
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           GenCore version (c) 1993 - 2005
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                                                                                                                         440 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA
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Pred. No. 2.7e-163;
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Plants and plant cells transformation
AMPA-N-acetyltransferase
Patent: US 6448476-A 29 10-SEP-2002;

Location/Qualifiers
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Sequence 29 from patent US 6448476.
AR229556.1 GI:27269172
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/mol_type="genomic DNA"
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llarity 94.5%;
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AACCTCCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAGGGAAGGGAAAGGGAAAGGGAAAGGGAAAGGGAAAGGGAAAGGGAAAGGACTCCTCGGATTCCATTGCCCAGCTATCTGTGACATAGTGGAAAAG
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1 (bases 1 to 661)
Fuchs, F.L., Kishore, G.M. and MacIntosh, S.C. Method for improving the efficacy of insect Patent: EP 0339009-A2 30 25-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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                                 428 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAA 487
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                                                                                                                           GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
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                                                                            GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
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                                                                                                             GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
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75.3%; Score 554; DB 6; Length 24
Best Local Similarity 94.5%; Pred. No. 2.7e-163;
Matches 586; Conservative 0; Mismatches 30; Indels
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Barry, G.F.
Plants and plant cells transformation 4 AMPA-N-acetyltransferase
Patent: US 6448476-A 31 10-SEP-2002;
Location/Qualifiers
                                                                                                                                                                                                                                            Sequence 31 from patent US 6448476. AR229557

    2436
    organism="unknown"
    mol_type="genomic DNA"

                                                                                                                                                             CATTTGGAGAGGACACGCTG 731
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                                              GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGTATCGTTCAAGATGCC
            GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                    Barry, G.r. Plant cells transformation to Plants and plant cells transformation to AMPA.M-acetyltransferase Patent: US 6448476-A 25 10-SEP-2002; Location/Qualifiers
                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                              Sequence 25 from patent US 6448476.
AR229554
AR229554.1 GI:27269170
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/wol_type="genomic DNA"
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AR229554
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Db 508 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 567  Qy 652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 711  Db 568 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 627  Qy 712 CATTTGGAGAGGACACGCTG 731  Db 628 CATTTGGAGAGGACACGCTG 647	RESULT 7 AR271019 LOCUS LOCUS LOCUS DEFINITION Sequence 15 from patent US 6501009. ACCESSION AR271019. VERSION VERSION AR271019.1 GI:29702285 SKYWORDS SOURCE Unclassified. NGANISM Unknown. ORGANISM Unknown. TITLE AUTHORS ROMANO.C.P. TITLE TITLE TOCURS TOURNAL PATENTE: US 65010094 15 31-DEC-2002; FEATURES 1. Location/Qualifiers JOURNAL AUTHORS AUTHO	Oy 116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175	Qy 176 CAGGTATCTGACATCATCAAAAGACAGTAGAAAAGGGAGGTGGCACCTACAAATGCC 235	Qy 236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG 295 	OY 296 ATGGACCCCACCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA 355 	QY 356 AGCAAGTGGATTGATGTGATTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411	OY 412 AACCTCCTGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGACAGTAGAAAA 471	QY 472 GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC 531	QY 532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCAGGGGGGCTCGTGGAAAAGGA 591	Qy 592 GACGTICCAACCACGTCTICAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651	Oy 652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 711
Db   148 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCAGGAGGATCGTGGAAAAGAA 507   S92 GACGTTCCAACGAGTGTTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651	Qy         712 CATTTGGAGGACACGCTG 731           Db         628 CATTTGGAGGACACGCTG 647           Bb         628 CATTTGGAGGACACGCTG 647           RESULT 6         AR271023           LOCES 1023         3469 bp DNA linear PAT 10-APR-2003           DEFINITION Sequence 23 from patent US 6501009.         AR271023           VERSION AR271023         AR2710289           ACCESSION AR271023         AR2710289           ACCESSION AR271023         GI:29702289           SOURCE Unknown.         Unclassified.           VOCASAISM Unknown.         Unclassified.           AUTHORS Romano.C.P.         Location/Qualifiers           JOURNAL Patent: US 6501009-A 23 31-DEC-2002;         Location/Qualifiers           JOURNAL SOURCE SOURCE LOCAGRACE         AUTHORS LOCAGRACE           JOURNAL PATENT SOURCE LOCAGRACE         Location/Qualifiers           JOURNAL SOURCE SOURCE LOCAGRACE         AUTHORS LOCAGRACE           Location/Qualifiers         Location/Qualifiers           SOURCE SOURCE LOCAGRACE         AUTHORS LOCAGRACE           Location/Qualifiers         Location/Qualifiers           AUTHOR SOURCE LOCAGRACE         AUTHOR LOCAGRACE           AUTHOR SOURCE LOCAGRACE         AUTHOR LOCAGRACE	Ouery Match 75.3%; Score 554; DB 6; Length 3469; Best Local Similarity 94.5%; Pred. No. 2.7e-163; Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;	Qy         116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175           Db         28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC 87	OY 176 CAGCTATCTGTCACTTCATCAAAGGACAGTAGAAAGGAAGG	OY 236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG 295	OY 296 ATGGACCCCACCACGAGGATCGTGGAAAAAGAAGACGTTCCAACGTCTTCAA 355	OY 356 AGCAAGTGGATTGATGTGATTGCAGTGAGACTTTTCAACAAGGGTAATATCGGGA 411	OY 412 AACCTCCTGGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471	OY 472 GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC 531	Qy         532         TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCAGGAGCAGCATCGTGGAAAAAAAA	Qy 592 GACGTICCAACCACGTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651

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3284 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAGGGTAATATCCGGA 3343
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                                                                                                                                                                                          unclassified.
unclassified.

I (bases 1 to 8012)

S Mannerloef,M., Tenning,P.P. and Steen,P.
Glyphosate resistant transgenic plants
Patent: JP 2001503280-A 1 13-MAR-2001;
NOVARTIS AG
OS Unidentified
PN JP 2001503280-A/1
PP 13-MAR-2001
PF 31-OCT-1997 US 60/112003
PR 31-OCT-1997 US 60/112003
PR 31-OCT-1997 US E0/112003
PR 31-OCT-1997 US FREEN PC C Strandedness: Double,
CC Strandedness: Double,
CC Topology: Linear;
FH Key Location/Qualifiers
FT Source 10.8012
FT Source 10.8012
FT Source 10.8012
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                                                                                 DNA
plants.
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                               Glyphosate resistant transgenic BD008400
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3644 CATTTGGAGAGACACGCTG 3663
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JP 2001503280-A/1.
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                                                                                                                                                  PAT 08-AUG-2001
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568 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 627
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Mannerloef, M., Tenning, P.Peter. and Steen, P.
Transgenic plants
Patent: US 6204436-A 1 20-MAR-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.3%; Score 554; DB 6; I 94.5%; Pred. No. 2.8e-163; ive 0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                           Sequence 1 from patent US 6204436.
AR143709
AR143709.1 GI:15104405
                                               628 CATTTGGAGAGGACACGCTG 647
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Best Local Similarity 94.5
Matches 586; Conservative
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                                 2347 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
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Local Similarity 94.5%; Pred. No. 2.8e-163;
les 586; Conservative 0; Mismatches 30;
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Mannerloef, M., Tenning, P. Peter. and Transgenic plants
Patent: US 6204436-A 5 20-WAR-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    1. .8418
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                   AR143713 8418 bp
Sequence 5 from patent US 6204436.
AR143713. GI:15104999
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                                                                       CATTTGGAGAGGACACGCTG
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AR143713
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GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
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Pred. No. 2.8e-163;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 8349)
Corbin,D.R. and Romano,C.P.
Wethods for transforming plants to express Cry2Ab
.delta.-endotoxins targeted to the plastids
Patent: US 6489542-A 16 03-DEC-2002;
                                                                                                                                                                                                            linear
                                                                                                                                                                                                            DNA
                                                                                                                                                                                                     8349 bp
Sequence 16 from patent US 6489542.
AR260588
AR260588.1 GI:27311143
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1. .8349
/organism="unknown"
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Matches 586; Conservative
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GACGITCCAACCACGICITCAAAGCAAGIGGAITGAIGIGATAICICCACIGACGIAAGG 651
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/mol_type="unassigned DNA"
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Sequence 4 from patent US 6204436.
AR143712. GI:15104998
                                                                                                                                                                                                                    CATTTGGAGAGACACGCTG 3642
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DEFINITION
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                                                                                                                                     PAT 31-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3383 GAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC 3442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATACGGGAAACCTCCTCGGATTCCATTGCC 175
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Pred. No. 2.8e-163;
0; Mismatches 30; Indels
                                                                                                                         BD008404 8418 bp DNA
Glyphosate resistant transgenic plants.
BD008404

    .8418
    /organism="unidentified"
/mol_type="genomic DNA"
    /db_xref="taxon:32644"

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75.3%;
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Best Local Similarity 94.5
Matches 586; Conservative
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                                                       GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassified.

1 (bases 1 to 8798)

Mannerloef, M., Tenning, P.Peter. and Steen, P.
Transgenic plants

Patent: US 6204436-A 4 20-MAR-2001;

Location/Qualifiers
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Discourt Co. Lile 190-A 19 24-APR-2001;

OS Unidentified
PN JP 2001112490-A/19
PP 24-APR-2001
PP 24-APR-2000
PP 24-APR-2000
PP 27-SEP-2000 US 2000272128
PR 29-APR-1987 US
PP 27-APR-1987 US
PP 29-APR-1987 US
PP 29-APR-2001 US
PP 
                                                            3493 GAAGGTGCCTACAAATGCCATCATTGCGATAAAGGAAAGGCATCGTTGAAGATGCC 3552
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                                                                                                                                                      3613 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGTATCTCCCACTGACGTAAGG 3672
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                                                                                                                                                                                                                             592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unclassified.
1 (bases 1 to 661)
Fiskehof, D.A., Fuchs, R.L., Labrik, P.B., Mcpherson, S.A. and
Perlak, F.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
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Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Vermin damage-resistant plant.
BD013916
BD013916 GI:22554245
JP 2001112490-A/19.
unidentified
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Matches 585; Conserv
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Best Local S
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                                                                        AGCAAGTGGATTGATGATGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
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TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
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Pred. No. 2.8e-163;
0; Mismatches 30; Indels
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31-0CT-1997 US 60/112003
MARIE MANNERLOEF, PAUL PETER TENNING, PER STEEN
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    .8798
/organism='Unidentified'

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I (bases 1 to 8798)

Mannerloef, M., Tenning, P. P. and Steen, P. Glyphosate resistant transgenic plants
Patent: JP 2001503280-A 4 13-MAR-2001;
NOVARTIS AG
OS Unidentified
ND 2001503280-A/4
PD 13-MAR-2001
PP 20-0CT-1998 JP 1999525342
PP 31-OCT-1999 JP 1999525342
PR 31-OCT-1997 US 60/112003
PI MARIE MANNERLOEF, PAUL PETER TENNING, PE CL Strandedness: Double;
CC Strandedness: Double;
CC Topology: Linear;
FT Gource 1. . 8798
FT Gource / Organism='Unidentifiers
                                                                                                                                                                                                                                                                                                                                      Glyphosate resistant transgenic plants.
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2001503280-A/4.
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ilarity 94.5%;
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                                                                                                                                                GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC 531
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Search completed: October 11, 2005, 17:46:12 Job time : 7677 secs

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Aav63741 plasmid p Aad01285 Rice tran Aad01285 Rice tran Aad15563 pMON33829 Aaa15564 pMON33829 Aaa15564 pMON33829 Aad5562 pMON33829 Aad676263 Promoter Aaq76263 Promoter Aaq7623 Vector pl Aav63725 Vector pl Aav63725 Vector pl Aav63725 Vector pl Aav63725 Vector pl Aas1764 plasmid p Aas17547 plasmid p Aas175875 Luciferas Abv75875 Luciferas Abv75875 Luciferas

Title: Perfect score:

Sequence:

nucleic

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Scoring table:

Searched:

Minimum DB Maximum DB

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New bi-directional promoter complex comprising a modified enhancer region including at least 2 enhancer sequences, and at least 2 core promoters, useful for enhancing or improving transcriptional activity of transgenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a bi-directional promoter complex comprising a modified enhancer region that includes at least 2 enhancer sequences, and
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .736
4.tag= a
Another complement of this sequence is also claimed in claim 9 as SEQ ID number 2"
                                                                                                                                                                                                                                                                                                                      Transgene expression related bidirectional dual promoter complex
                                                                                                                                                                                                                                                                                                                                       Bidirectional dual promoter complex; transcription; transgene; agronomic performance; transformation; ds.
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                                                                                                                AAD61789
ABX95185
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AAS17548
AAF81265
ADA44822
AAZ27627
ABV75873
ABV75875
AAC66931
                              AAV63734
AAA15563
AAA15564
AAQ68893
AAQ68893
AAV63723
AAV63724
AAV63725
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Gray DJ;
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Aad61790 Bt.cry3Bb
Abx95186 B. thurin
Adk98488 B thuring
Adk98490 B thuring
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Abs53105 Transgene
Aan81003 Enhanced
Aad01017 Expressio
Aad01015 Expressio
Aad01018 Expressio
Aad1018 Expressio
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Aaa15565 pWON30464
Aax57309 Sugar bee
Aax57308 Sugar bee
Aav53707 Nucleotid
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Abx95190 B. thurin
Aaz51642 Bacillus
                                                        ; Search time 1159 Seconds (without alignments) 3759.215 Million cell updates/sec
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       5.1.6
Compugen Ltd.
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       GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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AAN81003
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AAD01017
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(first entry)

29-NOV-2002

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at least 2 core promoters. The core promoters are on either side of the modified enhancer region in a divergent orientation. The bi-directional promoter complex is useful for enhancing tranecriptional activity of transgens to improve agronomic performance used in genetic transformation with plants. Vectors that include the bi-directional promoter complex may be used to express foreign genes in mammalian cells and in plant cells including dicots and monocots. This sequence represents a bidirectional dual promoter complex useful for enhancing transcriptional activity of transgenes
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Pred. No. 6.9e-232;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 735; Conservative
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ABS53105 standard; DNA; 1360 BP.

ABS53105 ID ABS5 XX RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New bi-directional promoter complex comprising a modified enhancer region including at least 2 enhancer sequences, and at least 2 core promoters, useful for enhancing or improving transcriptional activity of transgenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTTCAAAGCAAGTGGATTGATGTGTTGCAGTGAGACTTTTCAACAAAGGGTAATTG 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a bi-directional promoter complex comprising a modified enhancer region that includes at least 2 enhancer sequences, and at least 2 core promoters. The core promoters are on either side of the modified enhancer region in a divergent orientation. The bi-directional promoter complex is useful for enhancing transcriptional activity of transgenes to improve agronomic performance used in genetic transformation with plants. Vectors that include the bi-directional promoter complex may be used to express foreign genes in mammalian cells and in plant cells including dicots and monocots. This sequence represents a bidirectional goal promoter complex useful for enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          822 CATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAAGGTGGCACCTAC 881
                                                                                                                                                                                                                                  complement of this sequence is also claimed as SEQ ID number 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 AGAAGCTTCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         762 ATAAGCTTCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression related bidirectional dual promoter complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                            Bidirectional dual promoter complex; transcription; transgene; agronomic performance; transformation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1360 BP; 353 A; 319 C; 317 G; 371 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcriptional activity of transgenes
                                                                                                                                                                             Location/Qualifiers
1. .1360
/*tag= a
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                                                                                                                                                                                                                  /*tag= a
/note= "The c
in claim 10 a
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                                                                                                                                                  Synthetic
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                                                                                GCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACGAGGAGGATCGTGGGAAAAA 1241
                     TCTTCAAAGCAAGTGGATTGATGTGATTGCAGTGAGACTTTTCAACAAAGGGTAATATCG 1061
                                                                        GAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTA 648
                                                                                                                                 AGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTC 707
                                           AAGGAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGAT 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A fragment of the CaMV35S promoter (-343 to +9), previously constructed by Odell et al. (1985) Nature 313:810-812, is necessary for maximal expression of the promoter. It was exiced as a ClaI-HindIII fragment, made blunt ended with DNA pol I and inserted into the HincII site of
                                                   promoter;
                                                                                                                                                                                                                                Enhanced CaMV35S promoter used in pMON893 B.thuringiensis toxin prodn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetically transformed plants with toxicity to Coleopteran insects obtd. using chimeric gene contg. sequence encoding toxin protein of Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ε,
                                                                                                                                                                                                                                             Bacillus thuringiensis var. tenebrionis toxin gene; enhanced CaMV35S; pMON893; Coleopteran insects; transformed plants; chimaeric gene; ss.
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/note= "duplicated e
289. .541
/*tag= b
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/note= "duplicated
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                                                                                                                                                                                    AAN81003 standard; DNA;
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      199
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                     into the
promoter
AAN81000-
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                                                                                                                                                                                                                                                                       TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
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                                                                                                                                                                                                                                                                                                                                 ATGGACCCCCACCACCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA
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                                                                                                                                                                                                                                                TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CaWV35S promoter; Bacillus thuringiensis; toxin protein; insecticide; plasmid pMON893.
                                                                                                                                                                                                          Gaps
      this
into
                                                                                                                                                                                                            4,
pUC18. The upstream region of the 35S promoter was exiced from plasmid as a HindIII-ECRV fragment (-343 to -90) and inserted saame plasmid between the HindIII and PstI sites. The enhanced thus contains a duplication of sequences -343 to -90. See also
                                                                                                                                                                   Length 661;
                                                                                                                           Sequence 661 BP; 194 A; 160 C; 157 G; 150 T; 0 U; 0 Other;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enhanced CaMV35S promoter used in plasmid pMON893
                                                                                                                                                               Score 554; DB 1; L
Pred. No. 2.9e-172;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
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94.5%;
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                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cauliflower mosaic virus
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                                                                                                                                                             Query Match
Best Local Similarity
Matches 586; Conserv
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us-10-075-105c-1.rng

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619
     440 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA 499
                                        651
                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphonate herbicide tolerance; aminomethyl phosphonic acid; AMPA; acyltransferase; transacylase; recombinant plant; expression cassette; corn; tobacco; wheat; cotton; canola; rice; chloroplast transit peptide; CTP; glyphosate oxidase; GOX; glyphosate oxidoreductase; phnO gene; self-fertilisation; hetero-fertilisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acylrransferase (AAT) enzyme"
/function= "Transfers acyl group from an acylcarrier
(CoA) to the free amino group of aminomethylphosphonate"
                                                                                                                                                                                                                                                                                                                                                                                                                 Expression cassette-4 comprising modified E. coli P2A phnO coding gene.
                                      592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
                                                             500 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
                                                                                                             652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTATATAAGGAAGTTCATTT
                                                                                                                                 560 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  '*tag= a
'note= "Plant functional heterologous promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intracellular
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/product= "Escherichia coli modified P2A AMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/note= "Enhances expression of the phnO gene"
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/note= "Enhances expression of the phnO gene"
149. .1426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                               731
                                                                                                                                                                                                                  CATTTGGAGAGACACGCTG 639
                                                                                                                                                                                                                                                                                                         AAD01017 standard; DNA; 2107 BP.
                                                                                                                                                                                 CATTTGGAGAGGACACGCTG
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P-PSDB; AAY71251.
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                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barry GF;
                                                                                                                                                                               712
                                                                                                                                                                                                                                                                                                                                          AAD01017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
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                                                                                                                                                                                                                                                                    AAD01017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A fragment of the CaMV35S promoter (-343 to +9) in pUC13 was excised as a ClaI HindIII fragment and blunt-ended. This was inserted into the HinCII site of puC18. The upstream region of the 35S promoter was excised as a HindIII-ECORV fragment (extending from -143 to -90) and inserted into the same plasmid between the HindIII and PstI sites. The enhanced promoter thus contains a duplication of sequences between -343 ans -90. The promoter is used in plasmid pMON893 to express Bacillus thuringiensis toxin with a potentiating amt. of a trypsin inhibitor. This is useful as an insecticide. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAAGAAGATCCTTCCAACCACGTCTTCAA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACCICCICGGAIICCAIIGCCCAGCIAICIGICACIIIAAIIGIGAAGAIAGIGGAAAAG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCACGAGGAGGAGCATCGTGGAAAAAGAA 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                                              Toxin protein of Bacillus thuringiensis bacteria - improved in efficacy using a potentiating amt. of a trypsin inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCAAGTGGATTGATGTGAT ----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 554; DB 1; Length 661; Pred. No. 2.9e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 661 BP; 194 A; 160 C; 157 G; 150 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30; Indels
                                    /*tag= a
/note= "duplicated enhancer sequence"
                                                                                        /*tag= b
/note= "duplicated enhancer sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                          SC;
Location/Qualifiers
27. .279
                                                                                                                                                                                                                                                                                                                          Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 14; 56pp; English.
                                                                                                                                                                                                                  89EP-00870047
                                                                                                                                                                                                                                                    88US-00179709
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ilarity 94.5%;
Conservative
                                                                      .541
                                                                                                                                                                                                                                                                                                                          Kishore GM,
                                                                                                                                                                                                                                                                                     (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                             WPI; 1989-311431/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 586; Conser
                                                                                                                                                                                                                14-APR-1989;
                    misc_feature
                                                                        misc_feature
                                                                                                                                            EP339009-A.
                                                                                                                                                                                                                                                                                                                          Fuchs RL,
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The patent discloses a method for selectively enhancing the phosphonate and rice plants, by transforming the plants with an expression cassette. It comprises of a structural DNA sequence, that encodes an aminomethyl phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of Nacylation of AMPA. This sequence has an amino terminal chloroplast transit peptide (CTP), that targets AAT to the chloroplast Co-expression of glyphosate oxidase (GOX) gene, encoding glyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase, along with AAT provides the transformed plants with higher resistance to phosphonate herbicides. This method is useful for enhancing phosphonate herbicides such as glyphosate and AMPA tolerance, in recombinant plants and to prevent self-fettilisation and enhance hetero-fertilisation. The
                                                                                                                                                                                                                                                                                                    present DNA sequence is the expression cassette-1, comprising a plant operable promoter and 5' sequences like, 5' untranslated region (UTR) and intron, linked to modified E. coli phnO coding region encoding P2A AMPA acyltransferase (AAT) enzyme and plant operable termination sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCCACTGACGTAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
cotton, canola and rice plants involves transforming plants with phosphonate metabolizing genes encoding acyltransferase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4,
                                                                                                                                                                                                                                                                                                                                                                                                                          75.3%; Score 554; DB 3; Length 2107; 94.5%; Pred. No. 5.1e-172; ive 0; Mismatches 30; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2107 BP; 497 A; 531 C; 551 G; 528 T; 0 U; 0 Other;
                                                   Disclosure; Page 170-172; 179pp; English.
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586; Conservative
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The patent discloses a method for selectively enhancing the phosphonate herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola and rice plants, by transforming the plants with an expression cassette. It comprises of a structural DNA sequence, that encodes an aminomethyl phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of N-acylation of AMPA. This sequence has an amino terminal chloroplast transit peptide (CTP), that targets AAT to the chloroplast. Co-expression of glyphosate oxidase (GCX) gene, encoding glyphosate oxidoreductase, along with AAT provides the transformed plants with higher resistance to phosphonate herbicides. This method is useful for enhancing phosphonate
                                                                                                                                        acylransferase, transacylase, recombinant plant, expression cassette; corn; tobacco, wheat, cotton, canola; rice; chloroplast transit peptide; CTP; glyphosate oxidase; GOX; glyphosate oxidase; GOX; glyphosate oxidase; phnO gene; self-fertilisation; hetero-fertilisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acyltransferase (AAT) enzyme"
/function= "Transfers acyl group from an acylcarrier (COA) to the free amino group of aminomethylphosphonate" 1849. .2082
                                                                                                                           herbicide tolerance; aminomethyl phosphonic acid; AMPA; AAT;
                                                                                             Expression cassette-2 comprising modified E. coli P2A phnO coding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat, cotton, canola and rice plants involves transforming plants with phosphonate metabolizing genes encoding acyltransferase enzyme.
                                                                                                                                                                                                                                                                                           j. .bzv.
/tag= a
/note= "Plant functional heterologous promoter"
645. .715
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= d/ord="Targets the protein to an intracellular organelle, like chloroplast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= e
/product= "Escherichia coli modified P2A AMPA
                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/note= "Enhances expression of the phnO gene"
                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= c
/note= "Enhances expression of the phnO gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 164-166; 179pp; English.
                                                                                                                                                                                                                                                                       Location/Qualifiers
6. .620
BP
AAD01015 standard; DNA; 2122
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                                                           (first entry
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P-PSDB; AAY71251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-1998;
                                                             21-SEP-2000
                                                                                                                           Phosphonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-2000
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                               AAD01015;
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herbicides such as glyphosate and AMPA tolerance, in recombinant plants and to prevent self-fertilisation and enhance hetero-fertilisation. The present DNA sequence is the expression cassette-2, comprising a plant operable promoter and 5' sequences like, 5' untranslated region (UTR) and intron, linked to modified E. coli phno coding region encoding P2A AMPA acyltransferase (AAT) enzyme and plant operable termination sequences
                                                                                                                                                                                                        116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
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                                                                                                                                                                                                                                                                                                                                                                                               AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATAAAAGGACAGTAGAAAAG 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACGAGGAGGAGCATCGTGGAAAAAAA 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGITCCAACCACGICTTCAAAGCAAGIGGATIGAIGTGATAICTCCACIGACGIAAGG 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphonate herbicide tolerance; aminomethyl phosphonic acid; AMPA; AAT; acyltransferase; transacylase; recombinant plant; expression cassette; corn; tobacco; wheat; cotton; cannola; itce; chloroplast transit peptide; CTP; glyphosate oxidase; GOX; glyphosate oxidase; GOX; glyphosate oxidoreductase; phnO gene; self-fertilisation; hetero-fertilisation; ds.
                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expression cassette-5 comprising modified E. coli P2A phnO coding gene.
                                                                                                                                                                                                                          ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCAAGTGGATTGATGTGAT ----TGCAGTGAGACTTTTCAACAAGGGTAATATCGGGA
                                                                                                                                                                            4,
                                                                                                                                          75.3%; Score 554; DB 3; Length 2122; llarity 94.5%; Pred. No. 5.1e-172; Conservative 0; Mismatches 30; Indels
                                                                                                             Seguence 2122 BP; 495 A; 537 C; 561 G; 529 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      731
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                                                                                                                                                         al Similarity
586; Conserv
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The patent discloses a method for selectively enhancing the phosphonate herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola and rice plants, by transforming the plants with an expression cassette. It comprises of a structural DNA sequence, that encodes an aminomethyl phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of Nacylation of AMPA. This sequence has an amino terminal chloroplast transit peptide (GTP), that targets AAT to the chloroplast. Co-expression of glyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase, along with AAT provides the transformed plants with higher resistance to phosphonate herbicides. This method is useful for enhancing phosphonate herbicides such as glyphosate and AMPA tolerance, in recombinant plants and to prevent self-fertilisation and enhance hetero-fertilisation. The operable promoter and 5' sequences like intron, linked to modified E. Coli photo coding region, encoding PAA AMPA acyltransferase (AAT) enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCGATGTGAGACTTTTTCAACAAAGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC 87
                                                                                                                                                                                                                                                                     /product= "Escherichia coli modified P2A AMPA acyltransferase (AAT) enzyme" function= "Transfers acyl group from an acylcarrier (CoA) to the free amino group of aminomethylphosphonate" 2172. .2427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat, cotton, canola and rice plants involves transforming plants with phosphonate metabolizing genes encoding acyltransferase enzyme.
                                                                                         /*tag= a
/note= "Plant functional heterologous promoter"
670. .1473
                                                                                                                                                                                        /*tag= c
/note= "Targets the protein to an intracellular
organelle, like chloroplast"
                                                                                                                                   *tag= b
note= "Enhances expression of the phnO gene"
1498. 1725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.3%; Score 554; DB 3; L 94.5%; Pred. No. 5.5e-172; iive 0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 173-175; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             termination sequences
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/*tag= d
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Conservative
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plant operable
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Best Local Similarity
Matches 586; Conserv
                coli
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                Escherichia
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                                                                                                                                                                                                                                                                                                                                           terminator
                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is an expression cassette from a Cry3Bb plant expression vector pMON33748. It comprises an enhanced Cauliflower mosaic virus (CaMV) 355 promoter sequence, a wheat chlorophyll A/B binding protein untranslated leader sequence, a rice actin intron sequence, a Bacillus thuringiensis delta-endotoxin Cry3Bb variant 11231mv2 coding sequence and a wheat heat shock Hspl7 transcription termination and polyadenylation sequence. This expression cassette is used to improve expression of Cry3B variant protein in transgenic plants e.g. maize, to increase insecticidal activity against Coleopteran pests. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAAAAGAGGTTCCAACCACGTCTTCAA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327
                                                                                           /note= "Wheat heat shock Hsp17 transcription termination and polyadenylation sequence"
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                                                                                                                                                                                                                                                                                                                             Novel expression cassettes which express Bacillus thuringiensis Cry3 delta-endotoxin portion which is toxic to coleopteran insect pests, useful for producing transgenic plants with improved insecticidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.3%; Score 554; DB 3; Length 3469; 94.5%; Pred. No. 6.5e-172; tive 0; Mismatches 30; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;
      note= "Rice actin intron sequence"
                                         "Cry3Bb variant 11231mv2"
                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; Page 149-152; 171pp; English
                                                                   /*tag= e
/label= T-Ta.hsp17
                             /*tag= d
/product= "C1
3217. .3450
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                  .3202
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Matches 586; Conservative
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                                                        terminator
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ATGGACCCCCACCACGAGGAGCATCCTGGAAAAAGAAGCTCCAACCACCTCTTCAA
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                                        ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                       AGCAAGTGGATTGATGTGAT ----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA
                                                                                                                                                                   AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA
                                                                                                                                                                                              AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG
                                                                                                                                                                                                                                               GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC
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//label= P-CaMV.35S
664. .734
//tabel= L-Ta.hcbl
/note= "Wheat chlorophyll A/B binding protein
untranslated leader sequence"
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(first entry)
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Bacillus thu
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21-JUN-2000
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235 147 295 207 355 267

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B. thuringiensis delta endotoxin Cry3Bbl 11231mv2 expression cassette #2.
                                                                                                                   The invention relates to novel transgenic plants comprising Bacillus thuringiensis Cry3-delta-endotoxin gene or its variants having coleopteran inhibitory activity. The invention is useful for controlling coleopteran insect infestation in a field of crop plants. The present sequence is B. thuringiensis Cry3Bb-delta- endotoxin variant expression
                 comprises Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 AACCTCCTGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  568 GAIGACGCACAAICCCACTAICCTICGCAAGACCCTICCTCIAIAIAAGGAAGITCAITI
                                                                                                                                                                                                                                                                                                                                                                                                        116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 AGCAAGTGGATTGATGTGAT ----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA
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                                                                                                                                                                                                                                                                                                                    Length 3469;
                                                                                                                                                                                                                                                                        Sequence 3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                            Indels
                 New transgenic plant resistant to Coleopteran pests, thuringiensis Cry3-delta-endotoxin gene.
                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                           Query Match
75.3%; Score 554; DB 10;
Best Local Similarity 94.5%; Pred. No. 6.5e-172;
Matches 586; Conservative 0; Mismatches 30:
                                                                               Claim 16; Page 77-80; Opp; English.
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                                                                                                        GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCCACTGACGTAAGG
                                                                                                                                                                                                                                                                              GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
                                       GAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC
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GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC
                                                                               GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
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/note= "Cauliflower mosaic virus 35S promoter
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/*tsg= b
/note= "Wheat chlorophyll A/B binding protein
uranslated leader sequence (L-Ta.hcbl)"
748. .1238
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/note= "Rice actin intron (I-Os.Act1)"
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Chimeric - Oryza sativa.
Chimeric - Bacillus thuringiensis.
Chimeric - Triticum aestivum.
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25. .640
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/note= "Wheat h
and polyadenyla
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- Triticum aestivum.
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3217. .3420
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P-PSDB; ABW01055.
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The invention relates to a modified polynuclectide which encodes an insecticidal crystal 3 (Cry3) Bacillus thuringiensis delta-endotoxin such as CryBb. The modified polynuclectide is useful for producing a transformed cell, by introducing the modified polynuclectide into a cell such as a plant cell (preferably a maize cell) or a microbial cell. The modified polynuclectide is useful for producing a transformed maize plant cell and regenerating a maize plant by introducing the modified polynuclectide into a maize plant cell. Selecting a transformed maize plant cell. A transgenic plant expressing the modified polynuclectide is useful for controlling coleopteran insect infestation in a field of crop plants. The modified polynuclectide is useful for producing transgenic plants expressing higher levels of the insect controlling B. thuringiensis delta-endotoxin. The modified polynuclectide provides up to 10 fold higher levels of insect controlling Compositions. In particular, transgenic maize expressing higher levels of the Cry3Bb protein designed to exhibit increased toxicity toward to compositions. In particular, transgenic maize expressing higher levels of the Cry3Bb protein designed to exhibit increased toxicity toward to composition and pests dellares amperior levels of insect protection and are less likely to sponsor development of populations of target insects that are resistant to the insecticidally active protein. Improved control of
Cry3Bb1 11231mv2, gene, delta-endotoxin; plant, transgenic, insecticide, crystal 3; Cry3; Coleopteran insect infestation; increased toxicity; ds; season long protection; beetle; maize; rice; expression cassette.
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polyadenylation sequence"
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'note= "Rice actin intron"
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'note= "Enhanced CW35S promoter"
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3217. .3450
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Cauliflower mosaic virus.
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P-PSDB; ABU09202.
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susceptible target insect pests and season long protection from insect pathogens is achieved using the modified polynucleotide. The modified polynucleotide reduces the number of transgenic events that have to be screened in order to identify one which contains beneficial levels of one or more insect controlling compositions. The present sequence represents bacillus thuringiensis delta endotoxin Cry3Bbl 11231mv2 expression cassette #2 DNA
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                                                                                                                                                                                     4,
                                                                                                                                                       Length 3469;
                                                                                                                        756 T; 0 U; 0 Other;
                                                                                                                                                                                     Indels
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                                                                                                                                                   Score 554; DB 10;
Pred. No. 6.5e-172;
0; Mismatches 30;
                                                                                                                        Sequence 3469 BP; 790 A; 1078 C; 845 G;
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                                                                                                                                                     Query Match
Best Local Similarity 94.5%;
Matches 586; Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic plant, Cry3Bb-delta-endotoxin, Coleopteran pest resistance, insecticide, variant, cyclic, circular, chimeric, maize, gene, ds.
                                                                                                                                               AACCICCICGGATICCATIGCCCAGCIATCIGICACTITATIGIGAAGATAGIGGAAAAG
                                                                                                                                                                                        GAAGGTGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC
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                                                                                            AGCAAGTGGATTGATGTGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA
                                                                                                                     AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG
                                                                                                                                                                         GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC
                                                                                                                                                                                                                           TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA
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/note= "Cauliflower mosaic virus 35S promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Zea mays Hsp70 intron (I-Zm.Hsp70)
1490. .3451
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/product= "Bt.cry3Bb.v11231 protein"
3475. .3730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bt.cry3Bb.v11231 expression vector DNA, pMON33710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric - Cauliflower mosaic virus.
Chimeric - Zea mays.
Chimeric - Bacillus thuringiensis.
Chimeric - Agrobacerium tumefaciens.
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25. .640
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669. .1472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                             /label= T-AGRtu.nos
/note= "Agrobacterium tumefaciens nopaline synthase 3'
transcription termination and polyadenylation sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3754 BP; 1030 A; 889 C; 800 G; 1035 T; 0 U; 0 Other;
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/label= I-Zm.Hsp70
/note= "%ea mays Hsp70 intron sequence"
1490. .3451
                                                                                                                                                                                                                        "Cry3Bb variant AAV11231"
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/label= CaMV35S_promoter
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                                                                                           Location/Qualifiers
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                                    Bacillus thuringiensis.
Agrobacterium tumefaciens.
Chimeric.
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            Cauliflower mosaic virus.
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P-PSDB; AAY70444.
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                                                                                                                                                                                                  The invention relates to novel transgenic plants comprising Bacillus thuringlensis Cry3-delta-endotoxin gene or its variants having coleopteran inhibitory activity. The invention is useful for controlling Coleopteran insect infestation in a field of crop plants. The present sequence is B. thuringiensis Cry3Bb-delta- endotoxin variant expression
                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                       New transgenic plant resistant to Coleopteran pests, comprises Bacillus
                                                                                                                                                                                                                                                                                                                                                                                  28 TCCGATGTGAGACTTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC
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                                                                                                                                                                                                                                                                                          Sequence 3754 BP; 1030 A; 889 C; 800 G; 1035 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                   Length 3754;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                Score 554; DB 10;
Pred. No. 6.7e-172;
0; Mismatches 30;
                                                                                                                                                   thuringiensis Cry3-delta-endotoxin gene
                                                                                                                                                                            Claim 16; Page 57-60; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATTTGGAGAGGACACGCTG 731
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                                                                                                                                                                                                                                                                                                                   75.3%;
29-AUG-2002; 2002US-00232665
                         99US-00377466.
                                                                                                                                                                                                                                                                                                                                            Matches 586; Conservative
                                                                                                 2003-810928/76.
                                               (ROMA/) ROMANO C P.
                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                WPI; 2003-810928/
P-PSDB; ABW01053.
                         19-AUG-1999;
                                                                                                                                                                                                                                                                  vector DNA
                                                                         Romano CP;
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The invention relates to a modified polynucleotide which encodes an insecticidal crystal 3 (Cry3) Bacillus thuringiensis deltae-endotoxin such as CryBb. The modified polynucleotide is useful for producing a cell transformed cell, by introducing the modified polynucleotide into a cell such as a plant cell (preferably a maize cell) or a microbial cell. The modified polynucleotide is useful for producing a transformed maize plant by introducing the modified polynucleotide into a maize plant cell, selecting a transformed maize plant cell and regenerating a maize plant from the transformed maize plant cell A transgenic plant expressing the modified polynucleotide is useful for controlling Coleopteran insect infestation in a field of crop plants. The modified polynucleotide is useful for controlling transgenic plants expressing higher levels of the insect controlling B. thuringiensis delta-endotoxin. The modified polynucleotide provides up to 10 fold higher levels of insect controlling
                                                                                                                            Cry3Bbv11231; ds, gene, delta-endotoxin; plant; transgenic; insecticide; crystal 3; Cry3; Coleopteran insect infestation; increased toxicity; season long protection; beetle; maize; expression cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Agrobacterium tumefaciens nopaline synthase transcription terminator and polyadenylation sequence"
                                                                                              B. thuringiensis delta endotoxin Cry3Bb1v11231 expression cassette #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified polynuclectide useful for controlling Coleopteran insect infestation in a field of crop plants encodes insecticidal crystal 3 Bacillus thuringiensis delta-endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                         /cons_splice= (5'site:NO,3'site:NO)
/note= "Zea mays HSP70 intron"
                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "Enhanced CaMV35S promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Cry3Bblv11231"
3475. .3730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 105-110; 107pp; English.
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MONS ) MONSANTO TECHNOLOGY LLC.
BP.
ABX95186 standard; DNA; 3754
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/number= 1
                                                                 (first entry)
                                                                                                                                                                                                                                  Agrobacterium tumefaciens.
Cauliflower mosaic virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                    Bacillus thuringiensis.
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expression cassette DNA SeqID11

B thuringiensis crylBb-related

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delta-endotoxin relative to the highest levels obtained using prior compositions. In particular, transgenic maize expressing higher levels of the Cry3Bb protein designed to exhibit increased toxicity toward Coleopteran pests deliver superior levels of insect protection and are less likely to sponsor development of populations of target insects that are resistant to the insecticidally active protein. Improved control of susceptible target insect pests and season long protection from insect pathogens is achieved using the modified polynucleotide. The modified polynucleotide reduces the number of transgenic events that have to be screened in order to identify one which contains beneficial levels of one
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                                                                                                                                                                     or more insect controlling compositions. The present sequence represents Bacillus thuringiensis delta endotoxin Cry3Bblv11231 expression cassette
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                                                                                                                                                                                                                                                                                                                                                      Arcarrecgaraaaggaaaggccarcgrrgaagargccrcrgccgacagrggrcccaaag
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                                                                                                                                                                                                                                                                     Length 3754;
                                                                                                                                                                                                                                   Sequence 3754 BP; 1030 A; 889 C; 800 G; 1035 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                75.3%; Score 554; DB 10;
.larity 94.5%; Pred. No. 6.7e-172;
Conservative 0; Mismatches 30;
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This invention relates to a novel polynucleotide sequence optimised for expression of an insecticidal protein in a plant. The invention may be useful for the production of pesticides whilst the disclosed sequences may be used for gene therapy. The polynucleotide sequence and methods are useful in the control of lepidopteran insect pests, and for producing transgenic plants with the ability to resist insect infestations. The invention provides polynucleotide sequences with enhanced, improved and optimised expression in monocot and dicot plant species. The present sequence is that of a B thuringiensis crylBb expression cassette which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide sequence optimized for expression of an insecticidal protein in a plant, useful in the control of Lepidoptera insect pests, and for producing transgenic plants with the ability to resist insect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAAAAAGAAGGTCCTTCCAA
                                                                                                                                                                                /*tag= a
/product= "B thuringiensis crylBb variant protein"
                                                                ds,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                            insecticidal protein, plant; pesticide, gene therapy; lepidopteran insect pest, transgenic plant; insect infestation resistance, monocot; dicot, crylBb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.3%; Score 554; DB 12; 94.5%; Pred. No. 7.8e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 7.86
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 11; 138pp; English
                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          MONSANTO TECHNOLOGY LLC
                                                                                                                                                                                                                                                                                                                           29-AUG-2002; 2002US-0407428P.
                                                                                                                                                                                                                                                                                           26-AUG-2003; 2003WO-US026510
                                                                                                                                                             1241. .4933
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                          CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      related to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                             Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                          Romano
                                                                                                                                                                                                                                                                                                                                                                         (BOGD/) BOGDANOVA N N. (ROMA/) ROMANO C P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2004-269221/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 586; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-269221,
P-PSDB; ADK98489
                                                                                                                                                                                                                            WO2004020636-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infestations
                                                                                                                                                                                                                                                            11-MAR-2004
                                                                                                                 Synthetic.
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295

(first entry)

03-JUN-2004

ADK98488 ADK98488

ADK98488 ID ADK9 XX AC ADK9 XX DT 03-J

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This invention relates to a novel polynucleotide sequence optimised for expression of an insecticidal protein in a plant. The invention may be useful for the production of pesticides whilst the disclosed sequences may be used for gene therapy. The polynucleotide sequence and methods are useful in the control of lepidopteran insect pests, and for producing transgenic plants with the ability to resist insect infestations. The invention provides polynucleotide sequences with enhanced, improved and optimised expression in monocot and dicot plant species. The present sequence is that of a B thuringiensis crylBb expression cassette which is
                                                                                                                                                                                                                       TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                                                                                    ATCATTGCGATAAAGGAAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCGTCCCAAAG
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                                                                                                                                  Sequence 5600 BP; 1199 A; 1907 C; 1437 G; 1057 T; 0 U; 0 Other;
                                                                                                                                                          Length 5600;
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                                                                                                                                                          Score 554; DB 12;
Pred. No. 8.2e-172;
0; Mismatches 30;
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Job time : 1166 secs
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Best Local Similarity 94.5%;
Matches 586; Conservative C
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268 AGCAAGTGGATTGATGTGGATGTCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 327
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                      GAAGGTGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC
                                                                                                                               GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                        B thuringiensis crylBb-related expression cassette DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              insecticidal protein; plant; pesticide; gene therapy;
lepidopteran insect pest; transgenic plant;
insect infestation resistance; monocot; dicot; crylBb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 13; 138pp; English
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P-PSDB; ADK98491.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/027,998A
FILING DATE: 23-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.3%; Score 554; DB 3; I larity 94.5%; Pred. No. 7.8e-178; Conservative 0; Mismatches 30;
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US-09-377-466B-13
US-09-810-861B-3
US-09-810-861B-4
US-09-186-002-15
US-08-038-7684-1
US-08-038-7684-1
US-08-031-151-8
US-09-011-151-8
US-09-737-626A-30
US-09-737-626A-30
US-09-737-626A-29
US-09-737-628-31
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NAME: Patterson, Melinda L
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1400
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 661 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*
(cgn2_6/ptodata/1/ina/5B_COMB.seq:*
(cgn2_6/ptodata/1/ina/6A_COMB.seq:*
(cgn2_6/ptodata/1/ina/6B_COMB.seq:*
(cgn2_6/ptodata/1/ina/RECTUS_COMB.seq:*
(cgn2_6/ptodata/1/ina/RECTUS_COMB.seq:*
(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-441-340-29

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US-09-377-466B-13

US-09-182-117-1

US-09-182-117-1

US-09-182-117-1

US-09-182-117-5

US-09-182-117-5

US-09-182-117-5

US-09-182-117-5

US-09-182-117-4

US-09-434-039A-5

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Listing first 45 summaries
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Patent No. 6448476;
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.;
TITLE OF INVENTION: Phosphonate Metabolizing Plants;
FILE REFERENCE: 38-21(15303);
CURRENT APPLICATION NUMBER: US/09/441,340;
CURRENT FILING DATE: 1999-11-16;
EARLIER APPLICATION NUMBER: 60/108,763;
NUMBER OF SEQ ID NOS: 32;
SOFTWARE: Patentin Ver. 2.0;
SEQ ID NO 25
                                                                                                                                                                                               30;
                                                                                                                                                          Score 554; DB 3;
Pred. No. 1.5e-177;
0; Mismatches 30;
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Best Local Similarity 94.5%;
Matches 586; Conservative
             FEATURE:
NAME/KEY: CDS
LOCATION: (1427)..(1858)
FEATURE:
NAME/KEY: terminator
LOCATION: (1869)..(2102)
 (1149)..(1426)
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US-09-441-340-29
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NAME/KEY: promoter
LOCARITON: (26)..(590)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/09441340

patent No. 6448476

GENERAL INPORMATION:
APPLICANT: BARYY, GERARD F.

TITLE OF INVENTION: Phosphonate Metabolizing Plants
FILE REFERENCE: 38-24[15303]

CURENT APPLICATION NUMBER: US/09/441,340

CURENT APPLICATION NUMBER: 60/108,763

EARLIER FILING DATE: 1999-11-17

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 32

LENGTH: 2107
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FEATURE:
NAME/KEY: transit_peptide
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                               OTHER INFORMATION: Description of Artificial Sequence:expression OTHER INFORMATION: cassette comprising plant promoter linked to OTHER INFORMATION: cassette comprising plant promoter linked to OTHER INFORMATION: sequence encoding AMPA acetyl transferase linked OTHER INFORMATION: to termination sequence INFORMATION: to termination sequence LOCATION: (6)..(620)
FEATURE:
ILOCATION: (6)..(620)
FEATURE:
ILOCATION: (645)..(715)
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                       transit_peptide (1179)..(1406)
                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (1407)..(1838)
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: terminator
LOCATION: (1849)...(2082)
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(729)..(1178)
                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 110
US-09-441-340-25
                                                                                                                                                                                                                                                                    LOCATION:
FEATURE:
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LOCATION:
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NAME/KEY: t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:monocot
OTHER INFORMATION: expression cassette comprising plant operable
OTHER INFORMATION: promoter linked to an intron, a sequence coding
OTHER INFORMATION: sequence
OTHER INFORMATION: sequence
OTHER INFORMATION: sequence
OTHER INFORMATION: sequence
INFORMATION: sequence
INFORMATION: (640)
FRATURE:
INFORMATION: (1473)
FRATURE:
INFORMATION: (1725) .. (1725)
FRATURE:
INFORMATION: (1725) .. (1725)
FRATURE:
INFORMATION: (1726) .. (1727)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCAAGTGGATTGATGTGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA
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                                                                                                                                                                                           APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Plants FILE REFERENCE: 38-21(15303)
CURRENT APPLICATION NUMBER: US/09/441,340
CURRENT APPLICATION NUMBER: 05/108,763
EARLIER APPLICATION NUMBER: 60/108,763
EARLIER FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 554; DB 3; I
Pred. No. 1.6e-177;
0; Mismatches 30;
                                                                                                         US-09-441-340-31; Sequence 31, Application US/09441340; Patent No. 6448476; GENERAL INFORMATION:
CATTIGGAGAGACACGCIG 627
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 94.5%;
Matches 586; Conservative
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NAME/KEY: terminator
US-09-441-340-31
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296 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAAGAGGTTCCAACCACGTCTTCAA 355
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Patent No. 5501009
GENERAL INFORMATION
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in F.
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT ELING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 3754
                                                                                                                                                                                                                                                                388 GAAGGTGCTCTACAAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC
                                                                                                                                                                                                                                                                                                                                             116 TCTGCAGTGAGACTTTTCAACAAAGGTAATTCGGGAAACCTCCTCGGATTCCATTGCC
                               208 ATGGACCCCACCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA
                                                                             356 AGCAAGTGGATTGATGTGAT ---TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA
                                                                                                                     268 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGA
                                                                                                                                                             412 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG
                                                                                                                                                                                                                                                                                                                      532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCACGAGGAGCATCGTGGAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                      592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGTATCTCCACTGACGTAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           568 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
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COCATION: (25)..(640)

OTHER INFORMATION: P-CaMV.35S

NAME/KEY: intron

LOCATION: (669)..(1472)

OTHER INFORMATION: 1-Zm.Hsp70

NAME/KEY: CDS

OTHER INFORMATION: Cry3Bb1 variant v11231

OTHER INFORMATION: Gy3Bb1 variant v11231

OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription

OTHER INFORMATION: termination and polyadenylation sequence
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Best Local Similarity 94.5%; Pred. No. 2.1e-177;
Matches 586; Conservative 0; Mismatches 30;
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OTHER INFORMATION: Description
OTHER INFORMATION: cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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US-09-377-466B-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/09377466B
Patent No. 6501009
GENERAL INFORMATION:
APPLICANT: Romano, Charles P.
TITLE OF INVENTION:
FILE REFERENCE: 38-21 (15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/09/377,466B
CURRENT PILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                              447
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                                                                                              GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
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                                                                                                                                                         GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
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NAME/KEY promoter
LOCATION: (25)..(640)
OTHER INFORMATION: P-CaMV.35S
NAME/KEY: 5.UTR
NAME/KEY: 5.UTR
OCATION: (664)..(734)
OTHER INFORMATION: L-Ta.hcbl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DCCATION: (1241)...(3199)
OTHER INFORMATION: CLY3Bb1 variant 11231mv2
NAME/KEY: terminatch
LOCATION: (3217)...(3450)
OTHER INFORMATION: T-Ta.hsp17
                                                                                                                                                                                                                                                                                                                CATITGGAGAGACACGCTG 731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (748)..(1238)
OTHER INFORMATION: I-OS.ACt1
NAME/KEY: CDS
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Matches 586; Conservative
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3284 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTTCAACAAAGGGTAATATCCGGA 3343
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                                                                   3044 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC 3103
                                                                                                                                                                                                                                                                                                                                                                                                       3344 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 3403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3404 GAAGGIGGCICCIACAAAIGCCAICAIIGCGAIAAAGGAAAGGCCAICGIIGAAGAIGCC 3463
                                                                                                                                                                                        3164 ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3584 GAIGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT
                                                                                                                         236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                    296 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAAAAAGACGTTCCAACCACGTCTTCAA
                                                                                                                                                                                                                                                              3224 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAGAAGACGTTCCAACCACGTCTTCAA
                                                                                                   356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAGGGTAATATCGGGA
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     Gaps
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   30; Indels
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Sequence 1, Application US/09434039A

Patent No. 65316A9;
GENERAL INFORMATION:
APPLICANT: MANNERLOEF, Marie
APPLICANT: TENNING, Paul Peter
APPLICANT: TENNING, Per
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 09/434,039A
CURRENT FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/112,003
PRIOR APPLICATION NUMBER: 60/112,003
PRIOR APPLICATION NUMBER: 09/182,117
PRIOR APPLICATION NUMBER: 09/182,117
PRIOR APPLICATION NUMBER: 09/182,117
PRIOR APPLICATION NUMBER: 09/182,117
SEQ ID NO 1

LENGWARE: PatentIn version 3.0

SEQ ID NO 1

LENGWARE: PatentIN version 3.0
   Mismatches
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TCCGATGTGAGACTTTTCAACAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC 87
                                                                                                                  ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAAGAAGACGTTCCAACCACGTCTTCAA
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NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PatentIN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/182,117
FILING DATE:
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Patent No. 6204436
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8012 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: DNA (genomic)
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/182,117
FILING DATE:
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 Mismatches
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 8418 base pairs
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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; Sequence 16, Application US/09186002B
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; TITLE OF INVENTION: Improved Method for Transforming Plants to I;
TITLE OF INVENTION: delta-Endotoxins
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; CURRENT APPLICATION NUMBER: US/09/186,002B
; NUMBER OF SEQ ID NOS: 18
; NUMBER OF SEQ ID NOS: 18
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 30; Indels
Mismatches
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CATION: (3666)..(5573)
COTHER INFORMATION: completely synthesized
MS-09-186-002-16
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Conservative
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LENGTH: 8349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 711
                                                                                                                                                                                               ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACACAGTGCTCCCCAAAG
                                                                                                                                                                                                                                              236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                                                                                 296 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA
                                                                                                                                                                             GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
                                                                                                                                                                                                                                                                                                                                                                                   356 AGCAAGTGGATTGATGTGAT ----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC
                                                                                                        116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCAGGAGGAGCATCGTGGAAAAAGAA
                                                                          Gaps
                                                                          4 ;
                                       Length 8418;
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TITLE OF INVENTION: Transgenic Plant
MUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/182,117
                                                                        30; Indels
                                      Score 554; DB 4; I
Pred. No. 3.4e-177;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATTTGGAGAGACACGCTG 3642
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                                    75.3%;
ilarity 94.5%;
Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
                                      Query Match
Best Local Similarity
Matches 586; Conserv
   US-09-434-039A-5
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US-09-182-117-4
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                                                                                                     116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                           ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                                 ATGGACCCCACCACGAGGAGCATCGTGGAAAAAAGAAGACGTTCCAACCACGTCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                   AGCAAGTGGATTGATGTGAT ----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG
                                                                        Gaps
                                                                        4
                                  Length 8418;
                                                                  0; Mismatches 30; Indels
                                  Score 554; DB 3; I
Pred. No. 3.4e-177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09434039A; Batent No. 6531649; GENERAL INFORMATION:
APPLICANT: MANNERLOFF, Marie
APPLICANT: TENNING, Paul Peter
APPLICANT: STEEN, Per
TITLE OF INVENTION: Transgenic Plants; FILE REFERENCE: 09/434,039
CURRENT APPLICATION UNMBER: 08/09/434,039A; CURRENT FILING DATE: 1999-11-04; PRIOR APPLICATION NUMBER: 09/182,117
PRIOR FILING DATE: 1999-10-31; PRIOR PELING DATE: 1999-10-29; NUMBER OF SEQ ID NOS: 36; SOFTWARE: PatentIn version 3.0; SEQ ID NO 5; EENCHIN BALB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATTTGGAGAGACACGCTG 3642
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                                  Query Match
Best Local Similarity 94.5%;
Matches 586; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Sugar beet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-434-039A-5
US-09-182-117-5
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3313 Arggaccccaccaccacgaggagcarcgrggaaaaagaagacgrrccaaccacgrcrrcaa 3372
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                                                                                                                                                                                                3133 TCCGATGTGAGACTTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                                                                                     ATCATTGCGATAAAGGGAAAGGCTATCGATCAAGATGCCTCTGCCGACAGTGCTCCCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3373 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTTCAACAAAGGGTAATATCCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC
                                                                                                                                                                                                                                         3253 ATCATIGCGATAAAGGAAAGGCCATCGTIGAAGATGCCTCTGCCGACAGTGGTCCCAAAG
                                                                                                                                                                                                                                                                                                                                                                     ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAAGAAGACGTTCCAACCACGTCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA
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                                                                                                                                               Gaps
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US-07-936-163-46

i Sequence 46, Application US/07936163

i Patent No. 5743477

i GENERAL INFORMATION:

APPLICANT: MALSH, TERENCE A

APPLICANT: HOUTCHENS, ROBERT A

APPLICANT: HOUTCHENS, ROBERT A

APPLICANT: HOUTCHENS, ROBERT A

APPLICANT: ORR, GENEGORY L

ITILE OF INVENTION: INSECTICIDAL PROTEINS AND METHOD FOR

TITLE OF INVENTION: PLANT PROTECTION

NUMBER OF SEQUENCES: 49

CORRESPEDIBENCE ADDRESS:

ADDRESSE: THOMAS D. ZINDRICK

STREET: 9002 PURIONE ROAD

CITY: INDIANAPOLIS

STATE: IN
                                                                                                                                               4 ;
                                                                                                            Length 8798;
                                                                                                                                             Indels
                                                                                                                                               30;
                                                                                                              75.3%; Score 554; DB 4; I 94.5%; Pred. No. 3.4e-177;
                                                                                                                                             0; Mismatches
                                                                                                                                             Matches 586; Conservative
                               LENGTH: 8798
TYPE: DNA
ORGANISM: Sugar beet
                                                                                                                              Best Local Similarity
                                                                                JS-09-434-039A-4
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                                                                                                                                               Gaps
                                                                                                                                               4.
                                                                                                            Length 8798;
                                                                                                                                            30; Indels
                                                                                                            Score 554; DB 3; I
Pred. No. 3.4e-177;
0; Mismatches 30;
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Fatent No. 6531649
GENERAL INFORMATION:
APPLICANT: MANNERLOEF, Marie
APPLICANT: TENNING, Paul Peter
APPLICANT: STEEN, Per
FILE OF INVENTION: Transgenic Plants
FILE REPERENCE: 09/434,039
CURRENT FILING DATE: 1999-11-04
FRIOR APPLICATION NUMBER: 60/112,003
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 36
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PATENTIN VERSION 3.0
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TUPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                            75.3%;
94.5%;
                                                                                                            Query Match
Best Local Similarity 94.5
Matches 586; Conservative
                                                           ANTI-SENSE: NO
                ; TOPOLOGY:
; MOLECULE TYI
; HYPOTHETICA:
; ANTI-SENSE:
US-09-182-117-4
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US-09-434-039A-4
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NAME: Krueger, James P.
REGISTRATION NUMBER: 35,234
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
TELEPHAX: 312-372-7848
                                                                                                                                                                                                                                                                                                                                                                                                    35,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1030 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPPLOGY: unknown
WOLECULE TYPE: DNA (genomic)
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Best Local Similarity 93.2%;
Matches 588; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1030 base pairs
                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                               USA
                                                                                                                                                                                                                               60603
    RESULT 15
US-08-729-601A-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                13 CTGCAGATCTGCATGGGTGGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGG 72
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                                                                                                                                                                                                                                                                                                                                              Query Match 74.9%; Score 551.4; DB 1; Length 1030; Best Local Similarity 93.2%; Pred. No. 7.7e-177; Matches 588; Conservative 0; Mismatches 41; Indels 2;
ZIP: 46268-1189
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/936,163
FILING DATE: 27-AUG-1992
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 AGTTCATTTGGAGAGAGACACGGGGGA 643
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: ZINDRICK, THOMAS D
REGISTRATION NUMBER: 32,185
REFERENCE/DOCKET NUMBER: C-38,424A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-1869
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1030 BASE PAIRS
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                     ;
TOPOLOGY:
US-07-936-163-46
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                                                                               APPLICANT: Merlo, Donald J.
APPLICANT: Merlo, Donald J.
APPLICANT: Folkerts, Otto
TITLE OF INVENTION: Modified Bacillus Thuringiensis
TITLE OF INVENTION: Lepidopteran Control in Plants
TITLE OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 115 S. LaSalle St.
STREET: LL
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,601A
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Pred. No. 7.7e-177;
0; Mismatches 41;
Sequence 43, Application US/08729601A; Patent No. 6166302; GENERAL INFORMATION:
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Search completed: October 11, 2005, 14:58:23 Job time : 186 secs

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October 11, 2005, 12:54:20 ; Search time 718 Seconds (without alignments) 7139.448 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                       - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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736
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 1, Appli Sequence 3, Appli Sequence 29, Appl Sequence 25, Appl Sequence 25, Appl Sequence 31, Appl Sequence 31, Appl
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80	22 22 15 15 15 15
% Query Match Length DB ID	736 1360 661 2107 2122 2436 3469
% Query Match	100.0 81.2 75.3 75.3 75.3
Score	597.4 597.4 554 554 554 554 554
Result No.	

Appl	Appli	i, Appl	Appl	Appl	Appl	App1	Appli	Appli	Appl	Appl	ppli	Appli	ppli	Appli	Appl	Appl	Appli	Appli	Appli	Appl	Appli	Appl	Appl	Appli	Appl	Appl	Appli	Appl	Appl	Appl	Appli	Appli	Appl	Appl	Appl	Appl
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Seguence	Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
US-10-232-665-15 US-10-198-478-16	10-378-810	-10-759-602	-10-759-602	10-198-478-1	0-198-478	0-198-478	US-10-759-602-8	US-10-759-602-9	US-10-759-602-10	US-10-232-665-13		US-10-792-491-3	JS-09-810-861B-4	US-10-792-491-4	_	US-10-322-656-12	US-10-473-945-2	US-10-473-945-5	US-10-473-945-4	US-10-161-403-90	10-161-408-	11-006-076-	US-10-161-403-97	10-161-408-	11-006-076	US-10-161-403-92	US-10-161-408-3	US-11-006-076-92	_	10-161-403	10-161-408	-10-161-408	-11-006-076-8	-11-006-076-8	-10-161-4	US-10-161-403-95
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75.3		74.9							74.5	73.9	72.6		72.6	72.6	71.5	71.5	71.5	71.5	71.5	g	9	9	o,	8.69	σ	g,	σ	g	σ	69.8	σ	σ	σ	σ	9	σ
554	551.4	551.4	550.4	550	550	550	548.4	548.4	548.4	543.6	534.6	534.6	534.6	534.6	526	526	526	526	526	514	514	514	514	514	514	514	514	514	514	514	514	514	514	514	514	514
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## ALIGNMENTS

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Publication No. US20050188432A1

Publication No. US20050188432A1

Publication No. US20050188432A1

APPLICANTI Li, Zhijian T

APPLICANT: Gray, Dennis J

TITLE OF INVENTION: Bi-Directional Dual Promoter Complex with Enhanced Promoter Activ

TITLE OF INVENTION: Transgene Expression in Eukaryotes

FILE REFERENCE: 7270-72978

CURRENT APPLICATION NUMBER: US/10/075,105C

CURRENT FILING DATE: 2002-02-13

PRIOR TILING DATE: 2001-02-13

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 1

LENGTH: 736
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                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: CaMV 35S
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION:
US-10-075-105C-1
RESULT 1
US-10-075-105C-1
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APPLICANT: FISCHHOFF, DAVID A.
APPLICANT: FISCHHOFF, ROY L.
APPLICANT: FUCHS, ROY L.
APPLICANT: FISCHHOFF, ROY L.
APPLICANT: MCPHERSON, SYLVIA A.
APPLICANT: MCPHERSON, SYLVIA A.
APPLICANT: MCPHERSON, SYLVIA A.
APPLICANT: PERLAK, FREDERICK J.
TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
FILE REFERENCE: MOBEL: 195-108-31
CURRENT APPLICATION NUMBER: US/09/943,692
CURRENT FILING DATE: 1998-02-23
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PALENTIN Version 3.1
SEQ ID NO 33
LENGTH: 661
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US-09-943-692-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 AGAAGCTTCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTC
                                                                                                                                     ATAAAGCTTCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTC
                                                                                                                                                                                        AAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGT
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                                                                            Gaps
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                                         DB 22; Length 1360;
                                                                            Indels
                                     Score 597.4; DB 22;
Pred. No. 2.2e-191;
0; Mismatches 1;
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; Patent No. US20020152496A1
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ORGANISM: Artificial Sequence
                                     Query Match
Best Local Similarity 99.8%;
Matches 598; Conservative
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Sequence 3, Application US/10075105C
Publication No. US20050188432A1
GENERAL INFORMATION:
APPLICANT: Li, Zhijian T
APPLICANT: Gray, Dennis J
TITLE OF INVENTION: Bi-Directional Dual Promoter Complex with Enhanced Promoter Activ
TITLE OF INVENTION: Transgene Expression in Bukaryotes
FILE REFERENCE: 7270-72978
FILE REFERENCE: 7270-72978
CURRENT APPLICATION UNMERR: US/10/075,105C
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION UNMERR: 60/268,358
PRIOR APPLICATION UNMERR: 60/268,358
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
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                                                                                                              AGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCT 180
                                                                                                                                   TGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGA 300
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GGATCCAGCGTGTCCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTGCG 60
                                                                                                                                                                                      ATCTGTCACTTCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCAT
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                                     AAGGATAGTGGGATTGTGCGTCATCCCTTACGTCAGTGGAGATACTGCAGAAGCTTCTGC
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ORGANISM: CaMV 35S
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TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA
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OTHER INFORMATION: acetyltransferase, and termination sequence
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llarity 94.5%; Pred. No. 1.4e-176;
Conservative 0; Mismatches 30;
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US-10-213-791-25
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                                                                                                                                            ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG
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                                                         116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAAACCTCCTCGGATTCCATTGCC
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OTHER INFORMATION: Description of Artificial Sequence:expression
OTHER INFORMATION: cassette comprising plant operable promoter linked
OTHER INFORMATION: to a leader, intron, a sequence encoding an AMPA
                              Gaps
                               4 ;
 DB 9; Length 661;
Score 554; DB 9; Length 66
Pred. No. 8e-177;
0; Mismatches 30; Indels
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TITLE OF INVENTION: Phosphonate Metabolizing Plating FILE REFERENCE: 38-21(15303)
CURRENT APPLICATION NUMBER: US/10/213,791
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US/09/441,340
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/10213791 Publication No. US20030106096A1 GENERAL INFORMATION:
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                            Conservative
               Similarity
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Pred. No. 1.4e-176;
0; Mismatches 30; Indels 4
Publication No. US20030106096A1
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Phosphonate Metabolizing Plants
FILE OF INVENTION: Phosphonate Metabolizing Plants
CURRENT APPLICATION NUMBER: US/10/213,791
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US/09/441,340
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-17
NUMBER OF SEQ 1D NOS: 32
SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 94.5%;
Matches 586; Conservative
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// LOCATION: (1849)..(2082)
US-10-213-791-25
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LOCATION: (1407)..(1838)
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LENGTH: 2122
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; Sequence 31, Application US/10213791
; Bublication No. US20330106096A1
; GENERAL INFORMATION:
    APPLICANT: BATTY, Gerard F.
    TILE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION UNMBER: US/10/213,791
; CURRENT APPLICATION NUMBER: US/09/441,340
; PRIOR APPLICATION NUMBER: US/09/441,340
; PRIOR APPLICATION NUMBER: 05/09/41,340
; PRIOR FILING DATE: 1999-11-16
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 31
LENGTH: 2436
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94.5%; Pred. No. 1.5e-176;
iive 0; Mismatches 30;
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| LOCATION: (1498)..(1725)
| FEATURE:
| NAME/KEY: CDS
| LOCATION: (1726)..(2157)
| FEATURE:
| NAME/KEY: terminator
| LOCATION: (2172)..(2427)
| US-10-213-791-31
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LOCATION: (670)..(1473)
FEATURE:
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NAME/KEY: promoter
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APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REPERENCE: 38-21(15304) Cry3Bb Improved Exp.
CURRENT APPLICATION NUMBER: US/10/232,665
CURRENT APPLICATION NUMBER: US/09/377,466
PRIOR APPLICATION NUMBER: US/09/377,466
PRIOR PILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 15
LENGTH: 3754
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                                                                                                                                    Length 3469;
                                                                                                                                    75.3%; Score 554; DB 15;
llarity 94.5%; Pred. No. 1.9e-176;
Conservative 0; Mismatches 30;
OTHER INFORMATION: Cry3Bb1 variant 11231mv2 FEATURE:
NAME/KEY: terminator
LOCATION: (3217)..(3450)
OTHER INFORMATION: T-Ta.hsp17
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TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/232, 665

CURRENT PILING DATE: 1999-08-29

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATCHIN VET. 2.0

SOFTWARE: PATCHIN VET. 2.0

SOFTWARE: PATCHIN VET. 2.0
                                                                               296 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA 355
                                                                                                    208 ATGGACCCCCACCCACGAGGAGGAGCATCGTGGAAAAAAGAAGAGGTTCCAACCACGTCTTCAA 267
                                                                                                                                                           AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
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    236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG 295
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                          TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: expression
OTHER INFORMATION: cassette
OTHER INFORMATION:
LOCATION: (25)..(640)
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OTHER INFORMATION: P-CAMV.35S
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NAME/KEY: 5'UTR
LOCATION: (664)..(734)
OTHER INFORMATION: L-Ta.hcbl
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LOCATION: (748)..(1238)
OTHER INFORMATION: I-OS.Actl
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LOCATION: (1241)..(3199)
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                                                                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: (1490)..(3448)
OTHER INFORMATION: Cry3Bbl variant v11231
FEATURE:
NAME/KEY: terminator
LOCATION: (3475)..(3730)
OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
OTHER INFORMATION: termination and polyadenylation sequence
                        OTHER INFORMATION: Description of Artificial Sequence: expression OTHER INFORMATION: cassette
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                                                                                                                                                                                                                                                                            75.3%; Score 554; DB 15; Length 3754; larity 94.5%; Pred. No. 1.9e-176; Conservative 0; Mismatches 30; Indels 4
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                                               FEATURE:
NOME/KRY: promoter
LOCATION: (25)..(640)
OTHER INFORMATION: P-CaMV.35S
                                                                                                                     ION: (669)..(1472)
INFORMATION: I-Zm.Hsp70
ORGANISM: Artificial Sequence
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586; Conserv
                                                                                            FEATURE:
NAME/KEY: intron
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                                                                                                                     LOCATION:
OTHER INFO
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APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxy; FITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxy; FILE REFRENCE: 38-21 (13547) B
CURRENT APPLICATION NUMBER: US/10/198,478
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/186, 002
PRIOR PILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SEQ ID NOS: 18
SEQ ID NO 16
LENGTH: 8349
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Pred. No. 2.9e-176;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: completely synthesized
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Sequence 16, Application US/10198478
Publication No. US20030188336A1
GENERAL INFORMATION:
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Best Local Similarity 94.5%;
Matches 586; Conservative
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                                                                             APPLICATT: Rubin-Wilson, Beth
APPLICATT: Smith, Kelley A
APPLICATT: Smith, Kelley A
APPLICATT: Smith, Kelley A
TITLE OF INVENTION: PROMOTER AND INTRON FROM MAIZE ACTIN DEPOLYMERIZING
TITLE OF INVENTION: PACTOR
FILE REFERENCE: 50695
CURRENT APPLICATION NUMBER: US/10/378,810
CURRENT APPLICATION NUMBER: US 60/167,111
PRIOR PILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENT NET. 2.0
SEQ ID NO 2
LENGTH: 5796
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5796;
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US-10-378-810-2
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.9%; Score 551.4; DB 17; Length Best Local Similarity 93.2%; Pred. No. 1.8e-175; Matches 588; Conservative 0; Mismatches 41; Indels
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                                Sequence 2, Application US/10378810 Publication No. US20030213009A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
RESULT 10
US-10-378-810-2/c
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164 224 284 132 CTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAG 191 CACGICITICAAAGCAAGIGGAITGAIGIGAI - IGCAGIGAGACITITICAACAAAGGGIA 402 cacercricaaaccaaeresarrearerearearesaresacerriricaacaaassaa 311 TGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGAGGTTCCAAC 344 71 12 crecadarcracargastastastarcaacaaagastaararccasaaaccrccas CTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAG CTGCAGAAGCTTCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGG Gaps Woosley, Aaron TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants NUMBER OF SEQUENCES: 59 CORRESPONDENCE ADDRESS: Query Match
Past Local Similarity 93.2%; Pred. No. 1.9e-175;
Matches 588; Conservative 0; Mismatches 41; Indels 2; COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/759,602
APPLING DATE: 16-Jan-2004
CLASSIFICATION: «UDKNOWN» ; SEQUENCE DESCRIPTION: SEQ ID NO: 26: US-10-759-602-26 ADDRESSEE: DowAgroSciences LLC Sequence 26, Application US/10759602; Publication No. US20040143868A1 GENERAL INFORMATION:
APPLICANT: Ainley, Michael
Belmar, Scott
Folkerts, Otto
Hopkins, Nicole
Menke, Michael A.
Pareddy, Dayakar
Petolino, Joseph F.
Smith, Kelley STREET: 9330 Zionsville Road NAME: Kraus, Eric J TELECOMMUNICATION INFORMATION: TELEPHONE: 317 337 5110 TELEFAX: 317 337 4847 INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: ZIP: 46268 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk ATTORNEY/AGENT INFORMATION: TYPE: nucleic acid STRANDEDNESS: double CITY: Indianapolis STATE: Indiana TOPOLOGY: circular MOLECULE TYPE: DNA COUNTRY: USA

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74.8%;
 Query Match
Best Local Similarity 93.2
Matches 587; Conservative
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NAME/KEY: misc_feature
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                                                                                                                                                   GAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACT
                                                 GTAGAAAAGGAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTT
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TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/759,602
FILING DATE: 16-Jan-2004
CLASSIFICATION: CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 AGTICATITCATITGGAGAGGACACGCIGGA 733
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MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
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STREET: 9330 Zionsville Road
CITY: Indianapolis
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Armstrong, Katherine
Belmar, Scott
Folkerts, Otto
Hopkins, Nicole
Menke, Michael A.
Pareddy, Dayakar
Petolino, Joseph F.
Smith, Kelley
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TELECOMMUNICATION INFORMATION:
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US-10-759-602-19
US-10-759-602-19;
Sequence 19, Application US/10759602
Publication No. US20040143868A1
GENERAL INFORMATION:
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TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 19:
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LENGTH: 9335 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COUNTRY: USA
ZIP: 46268
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APPLICANT: Corbin, David R.
APPLICANT: Corbin, David R.
APPLICANT: Corbin, Charles P.
TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxy
TITLE OF INVENTION: IMproved Methods for Transforming Plants to Express delta-Endotoxy
TITLE OF INVENTION: IMPRES: US10/198,478
CURRENT APPLICATION NUMBER: US10/198,478
PRIOR PILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
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                                                              Gaps
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Length 9335;
                                                        Indels
  DB 19;
                                                              41;
Score 550.4; DB 19
Pred. No. 5.1e-175;
0; Mismatches 41;
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74.7%; Score 550; DB 16;
Best Local Similarity 94.5%; Pred. No. 7.3e-175;
Matches 582; Conservative 0; Mismatches 30;
                                                                                                            FEATURE:
OTHER INFORMATION: completely synthesized
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   PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
                                                                               TYPE: DNA ORGANISM: artificial sequence
                                                                                                                                       FEATURE:
NAME/KEY: misc feature
LOCATION: (1). (10312)
OTHER INFORMATION:
                                                SEQ ID NO 15
LENGTH: 10312
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Publication No. US20030188336A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Corbin, Charles P.
TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox FILE REPERENCE: 38-21 (13547) B
CURRENT FILING DATE: 2002-111-12
PRIOR APPLICATION NUMBER: 09/186, 002
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74.7%; Score 550; DB 16; Length 10249;
Best Local Similarity 94.5%; Pred. No. 7.3e-175;
Matches 582; Conservative 0; Mismatches 30; Indels 4;
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NAME/KEY: misc feature

LOCATION: (3597)..(3670)

OTHER INFORMATION: "n" = g,

FEATURE:

NAME/KEY: misc feature

LOCATION: (4292)..(4344)

GOTHER INFORMATION: "n" = g,
LOCATION: (1)..(10249)
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                                                                                                               APPLICANT: Corbin, David R.
APPLICANT: Corbin, David R.
APPLICANT: Romano, Charles P.
TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox FILE REPERBNCE: 38-21 (13547) B
CURRENT APPLICATION NUMBER: US/10/198,478
CURRENT FILING DATE: 2002-11-12
PRIOR PILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SEQ ID NO : 31
SEQ ID NO : 31
LENGTH: 10339
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OTHER INFORMATION: completely synthesized
FEATURE:

NAME/KEY:

NAME
US-10-198-478-13
; Sequence 13, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: artificial sequence
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Matches 582, Conservative
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        652 GAIGACGCACAATCCCACTATCGCAAGACCCTTCCTCTATATAAGGAAGTTCATT
        711

        Db
        559 GAIGACGCACAATCCCACTATCGTCGCAAGACCTTCTCTCTATATAAGGAAGTTCATTT
        618

        QY
        712 CATTTGGAGAGGACAC
        727

        Db
        619 CATTTGGAGAGGACAC
        634
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Search completed: October 11, 2005, 15:38:12 Job time : 722 secs

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CK438483 GQ0085.BR
CG472768 GQ0081.BR
CK437926 GQ0081.BR
CK437920 GQ0081.BR
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CK4378348 GQ0085.BR
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GG805017 1118056D1
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                                                                                   ; Search time 3213 Seconds (without alignments) 8719.360 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                      - nucleic search, using sw model
                                                                                   October 11, 2005, 14:58:28
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/tissue_type="Vascular cambium, secondary phloem and bark of trees girdled by removing a ring of bark ca. 1 cm wide from the midpoint of the main stem."

/dev_stage="Vascular cambium, secondary phloem, and bark from trees harvested 1 and 7 days after girdling
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                     Paule, C., Seguin, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
                                                                                                                                                                                                                                               Center for Computational Genomics and Bioinformatics (CCGB), University of Minnesota, MN id Identifier: MNS19113 Clone ID: GQ0081.BR K09 Clones available through: John MacKay, Ph. D. Professeur adjoint -Assistant professeur EMAIL: jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere
                                                                                                                                                                                                                                                                                                                                                    (Forest Biology Research Center) Universite Laval Quebec, Quebec CANADA GIK 7P4
                                                                                                                                                                                        CANADA G1K 7P4
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Moremcy,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., S
Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
Siddiqui,A., Holt,R., Marra,M. and MacKay,J.
Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
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Pavillon Charles Eugene Marchand,
Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
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/organism="Picea glauca"
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/strain="pg-653"
/db_xref="taxon:3330"
/clone="GQ0081.BR_K09"
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primer: M13 Reverse Primer.
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                                                                                                                           Contact: John MacKay
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.
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                              /note="Organ: Main stem of 4 year old saplings, approximately 60 cm tall; Vector: pBluescript II SK (+) xR; Site_1: Eco-H; Site_2: xho.1; Tissues were pooled from above and below the girdle. cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electropoxation into DH10B cells (In vitxogen) for propagation"
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GQ008B.BR.1 K09 GQ008: Cambium, phloem and bark of girdl
Picea glauca cDNA clone GQ0081.BR_K09 5', mRNA sequence.
CO472768
/clone_lib="GQ008: Cambium, phloem and bark of
                                                                                                                                                                                                                                                      Length 698;
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                                                                                                                                                                                                                                    Score 546.6; DB 7;
Pred. No. 1.8e-160;
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1 (bases 1 to 803)
Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A.,
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                                                                                                                                                           Length 755;
                                                                                                                                                                                          Indels
                                                                                                                                                           Score 546.6; DB 7;
Pred. No. 1.9e-160;
0; Mismatches 29;
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Best Local Similarity 94.7%;
Matches 577; Conservative
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Pavillon Charles Eugene Marchand, Quebec, Quebec, CANADA GIK 7P4
Pavillon Charles Eugene Marchand, Quebec, Quebec, CANADA GIK 7P4
Pax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesora MN id Identifier: MNS13701 Clone ID:
GQ0083_H02 Clones available Through: John MacKay, Ph. D. Professeur
adjoint _Assistant professor EMAIL: jmackay@rsvs, ulaval.ca Centre
adjoint _Assistant professor EMAIL: jmackay@rsvs, ulaval.ca Centre
center) Universite Laval Quebec, Quebec CANADA GIK 7P4
Plate: 3 row: 02 column: H
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Picea glauca
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

1 (bases 1 to 755)
Norency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A., Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
Siddiqui,A., Holt,R., Marra,M. and MacKay,J.
Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
Contact: John MacKay
Contract: John MacKay
Contract: John MacKay
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/dev stage="Vascular cambium, secondary phloem, and bark from trees harvested 1 and 7 days after girdling
CCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGAC 568
                                                                                                                                                                                                                                     CCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGAC 657
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Cambium, phloem and bark of girdled
                                                                                                                               GGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCC
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/mol_type="mRNA"
/strain="pg-653"
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Seg primer: M13 Reverse Primer.
Location/Qualifiers
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/sex="Hermaphrodite"
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/clone_lib="GQ008:
saplings"
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CK438332
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CO472761 803 bp mRNA linear EST 09-JUL-2004 GQ0081.BR.1 G07 GQ008: Cambium, phloem and bark of girdled saplings Picea glauca cDNA clone GQ0081.BR\_G07 S', mRNA sequence. CC472761.1 GI:S0141306 180 240 300 360 657 717 151 211 271 417 331 477 391 537 597 511 571 631 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea. 1 (bases 1 to 803) 451 /note="Organ: Main stem of 4 year old saplings,
approximately 60 cm tall; Vector: pBluescript II SK (+)
Kr, Site=1: Eco-RI; Site\_2: Xho-I; Tissues were pooled
Krom above and below the girdle. cDNA was prepared from 5
mg of poly A+ selected RNA and was directionally ligated
into the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (In
vitrogen) for propagation. 91 CCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGAC ATTGAGACTTTTCAACAAAGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCAGCT 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCAT ATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAATGCCATCAT TGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGA TGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCCAAAGATGGA CCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACCACCTTCAAAGCAA GACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTT 121 AGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCT CCCCCACCCACGAGGAGCATCGTGGAAAAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA GTGGATTGATGTGATTG---CAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTC Gregarricarerearecregarricacarricacaracaacaraarecregaaacere GGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCC Gaps

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Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA GIK 7P4

Fax: 418 656 7493

Bmail: jmackay@rsvs.ulaval.ca

Email: jmackay@rsvs.ulaval.ca

Center for Computational Genomics and Bioinformatics (CCGB),

University of Minnesota, MN_id Identifier: MN5171860 Clone ID:

GQ0081 K09 Clones available through: John Mackay, Ph. D. Professeur
adjoint Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
de Recherche en Biologie Forestiare (Forest Biology Research

Center) Universite Laval Quebec, Quebec CANADA GIK 7P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CK437984 713 bp mRNA linear EST 08-JAN-2004 GQ0081.BR K09 GQ008: Cambium, phloem and bark of girdled saplings Picea glauca cDNA clone GQ0081_K09 5', mRNA sequence.
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/dev stage="Vascular cambium, secondary phloem, and bark from trees harvested 1 and 7 days after girdling
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
1 (bases 1 to 713)
Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Morency, M.-J., Butterfield, Y., Barber, S., Yang, G., Stott, J., Siddiqui, A., Holt, R., Marra, M. and Mackay, J.
Arborea EST sequencing in Picea glauca (white spruce)
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/clone_lib="GQ008: Cambium, phloem and bark of girdled
                                                                      391 GGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCC
                                                                                                                                                                                                                                                                                                                                                                                GGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCC
                                                                                                                                          511 CCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGAC
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/mol_type="mRNA"
/strain="pg-633"
/db_xref="taxon:3330"
/clone="GQO081_K09"
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Seg primer: M13 Reverse Primer.
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                                                                                                                                                          Universite Laval

Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA GIK 7P4

Fax: 418 657 7493

Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MNS198052 Clone ID:
GQ0081.BR GG7 Clones available through: John MacKay, Ph. D.
Professeur adjoint -Assistant professor EMAII:
jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere
(Forest Bàology Research Center) Universite Laval Quebec, Quebec
CANADA GIK 7P4

Flate: 1.BR row: 07 column: G
Seq primer: MJ3 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      approximately 60 cm tall; Vector: pBluescript ISK (+) XR; Site_1: Bco-RI; Site_2: Xho-I; Tissues were pooled from above and below the girdle. cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (In vitrogen) for propagation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Wascular cambium, secondary phloem and bark of trees girdled by removing a ring of bark ca. 1 cm wide from the midpoint of the main stem"

/dev_stage="Vascular cambium, secondary phloem, and bark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCCACCTACAAATGCCATCAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCCCACCCACGAGGAGCATCGTGGAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crcegarrecarreccaecrarcrercacrrrarrergaagaracregaaaaaaggaaggr 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTGAGACTTTTCAACAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCT 90
                                                                                                                                                                                                                                                                                                                                                                                Forestiere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="GQ008: Cambium, phloem and bark of girdled
saplings"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCTGTCACTTTATTGTGAAAGGAAAGGAAAGGAAGGTGGCTCCTACAAATGCCATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Vascular cambium, secondary phloem, e
from trees harvested 1 and 7 days after girdling
Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J., Siddiqui, A., Holt, R., Marra, M. and MacKay, J. Arborea EST sequencing in Picea glauca (white spruce) Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          э
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                               Contact: John MacKay
Centre de Recherche en Biologie Forestiere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.3%; Score 546.6; DB 7; 94.7%; Pred. No. 1.9e-160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. coli DH10B cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Picea glauca"
/mol_type="mRNA"
/strain="pg-653"
/db_xref="taxon:3330"
/clone="GQ0081.BR G07"
/sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment"
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GQ0083.BR J24 GQ008: Cambium, phloem and bark of girdled saplings
Pices glauca cDNA clone GQ0083_J24 5', mRNA sequence.
CK438362
                                                                                                                                                                                                                                                                                                  ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCCACCTACAAATGCCATCAT 240
                                                                                                                                                                                                                                                                                                                                                                             300
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1 (bases 1 to 741)

Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J., Siddiqui, A., Holt, R., Marra, M. and MacKay, J.
                                                                                                                                                                                                                                                                                                                                     Arcrercactriarrergaagaractegaaaaggaageregerecracaareccarcar 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCCCACCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGATTGATGTGATTG----CAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTC 417
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                                                                                                                                                                                                                         121 AGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCT
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                                                                                                                                                                                        Gaps
                                                                                                                                                    Length 713;
                                                                                                                                                                                        Indels
                                                                                                                                                    544.6; DB 7;
No. 7.8e-160;
                                                                                                                                                  ; Score 544.6; D; Pred. No. 7.8e-0; Mismatches
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Picea glauca
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94.4%;
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Best Local Simil
Matches 575; (
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KEYWORDS
SOURCE
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CK438362
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Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA GIK 7P4
Pax: 418 656 7493
Bmail: jmackay@revs.ulaval.ca
Bmail: jmackay@revs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN_id Identifier: MN5173771 Clone ID:
GQOGB3_U34 Clones available Through: John MarKay, Ph. D. Professeur
adjoint -Assistant professor EMALI: jmackay@revs ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA GIK 7P4
Seq primer: M13 Reverse Primer.
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ARP, Site 1: ECO-RI; Site 2: Xho-I; Tissues were pooled
from above and below the girdle. cDNA was prepared from so of poly A+ selected RNA and was directionally ligated
into the pBluescript IS K (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (In
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/tissue type="Vascular cambium, secondary phloem and of trees girdled by removing a ring of bark ca. 1 cm ifrom the midpoint of the main stem"
/dev_stage="Vascular cambium, secondary phloem, and b from trees harvested 1 and 7 days after girdling
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/clone_lib="GQ008: Cambium, phloem and bark of
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       spruce)
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llarity 94.4%; Pred. No. 7.9e-160;
Conservative 0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vitrogen) for propagation"
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Picea glauca"
/mol_type="mRNA"
/strain="pg-653"
/db_xref="taxon:3330"
                                                                 en Biologie
  in Picea
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                                           Contact: John MacKay
Centre de Recherche e
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CK438485 T36 bp mRNA linear EST 08-JAN-2004 GQ0085.BR_M24 GQ008: Cambium, phloem and bark of girdled saplings Picea glauca cDNA clone GQ0085_M24 5', mRNA sequence.
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1 (bases 1 to 736)

Morency, M. -J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J., Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
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  XR vector (Stratagene), into DH10B cells (In
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                                                                                                     655;
                                                                                                     Length
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                                                                                              Score 537.2; DB 7;
Pred. No. 1.6e-157;
0; Mismatches 43;
into the pBluescript II SK (+) transformed by electroporation vitrogen) for propagation"
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Picea glauca
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                                                                                                 Query Match
Best Local Similarity 92.5%;
Matches 567; Conservative
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Fax: 418 656 7493

Email: jmackay@rsv.ulaval.ca

Email: jmackay@rsvs.ulaval.ca

Center for Computational Genomics and Bioinformatics (CCGB),

University of Minnesota, MN id Identifier: MN5171736 Clone ID:

GQOGAL FOS Clones available Through: John Mackay, Ph. D. Professeur

adjoint -Assistant professor EMALI: jmackay@rsvs.ulaval.ca Centre

Geneter) Universite Enval Quebec, Quebec CANADA GIK 7P4

Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                        GQ0081.BR_F05 GQ008: Cambium, phloem and bark of girdled saplings Picea glauca cDNA clone GQ0081_F05 5', mRNA sequence. CK437920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bica glauca

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

(bases 1 to 655)

Morency, M. -J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J., Arborea EST sequencing in Picea glauca (white spruce)

Unpublished (2004)

Contact: John MacKay

Centre de Recherche en Biologie Forestiere
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/tissue_type="Vascular cambium, secondary phloem and bark
/tissue_type="Vascular cambium, secondary phloem and bark
of trees girdled by removing a ring of bark ca. 1 cm wide
from the midpoint of the main stem"
/dev_stage="Vascular cambium, secondary phloem, and bark
from trees harvested 1 and 7 days after girdling
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/lab_host="E. coli DH10B cells"
/clone_lib="GQ008: Camblum, phloem and bark of girdled
                                                                                                                                                                                                                        397 GGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCC
                                         CCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGAC
                                                                                                                                            CCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCCACTGACGTAAGGGATGAC
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/mol_type="mRNA"
fstrain="pg-653"
/db_xref="taxon:3330"
/clone="GQ0081_F05"
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AUTHORS
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
CK437920
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519

579

657

EST 08-JAN-2004

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Fax: 418 656 7493
Email: jmackay@revs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MNS174387 Clone ID:
GQ0085 D16 Clones available through: John MacKay, Ph. D. Professeur
adjoint -Assistant professor EMAIL: jmackay@revs.ulaval.ca Centre
de Recherche en Biologie Forestiare (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
Plate: 5 zow: 16 column: D
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

1 (bases 1 to 698)
Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A., Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A., Siddiqui,A., Holt,R., Marra,M. and MacKay,J.
Arborea EST sequencing in Picea glauca (white spruce)
Contact: John MacKay
Contre de Recherche en Biologie Forestiere
                                                                                                                                                                                                                                                                                                                                                                      698 bp mRNA linear EST 08-JAN-201 GQ0085.BR D16 GQ008: Cambium, phloem and bark of girdled saplings Picea glauca cDNA clone GQ0085_D16 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: Main stem of 4 year old saplings,
papproximately 60 cm tall; Vector: pBluescript II SK (+)
XR; Site_1: ECO-RI; Site_2: Xho-I; Tissues were pooled
from above and below the girdle. CDNA was prepared from 5
mg of poly A+ selected RNA and was directionally ligated
into the pBluescript II SK (+) XR vector (Stratagene)
transformed by electroporation into DH10B cells (In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. coli DH10B cells"
/clone_lib="GQ008: Cambium, phloem and bark of girdled
saplings"
                                                                                                             CCAACCACGTCTTCAAAGCAAGTGGATTGATGTGTTCTCCACTGACGTAAGGGATGAC
  658 GCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATAAAGGAAGTTCATTTCA 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="Vascular cambium, secondary phloem and of trees girdled by removing a ring of bark ca. 1 cm from the midpoint of the main stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Vascular cambium, secondary phloem, trom trees harvested 1 and 7 days after girdling treatment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 533.2; DB 7;
Pred. No. 3e-156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vitrogen) for propagation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Picea glauca"
/mol_type="mRNA"
/krain="pg-653"
/db xref="taxon:3330"
/clone="GQ0085_D16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Picea glauca (white spruce)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CK438348.1 GI:40769405
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94.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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JOURNAL
COMMENT
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CK438348
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KEYWORDS
SOURCE
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                                                                                               Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MNS174611 Clone 1D:
G00085 M24 Clones available through: John MacKay, Ph. D. Professeur
adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
Center) Universite Laval Quebec, Quebec CANADA GIK 7P4
Seq primer: M13 Reverse Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_trype="vascular cambium, secondary phloem and bark of trees girdled by removing a ring of bark ca. 1 cm wide from the midpoint of the main stem"
/dev stage="vascular cambium, secondary phloem, and bark from trees harvested 1 and 7 days after girdling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 TGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGGTCCCAAAGATGGA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 Arcretcacritaritergaagaracregaaaaggaaggregerecracaaargccarcar 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCCAAAGATGGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCCCACCACGAGGAGCATCGTGGAAAAAAAGACGTTCCAACCACGTCTTCAAAGCAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGATTGATGTGATTG----CAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 Gregarrearerearecrearreadacrirreaacaaagegraaraceegaaaccre 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 GCTCCTACAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: Main stem of 4 year old saplings,
approximately 60 cm tall; Vector: pBluescript II SK (+)
AR; Site_1: Eco-RI; Site_2: Xho-I; Tissues were pooled
from above and below the girdle. cDNA was prepared from 5
mg of poly A+ selected RNA and was directionally ligated
into the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (In
vitrogen) for propagation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCT 99
Centre de Recherche en Biologie Forestiere
Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA GIK 7P4
Fax: 418 656 7493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="GQ008: Cambium, phloem and bark of girdled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 535.2; DB 7;
Pred. No. 7.1e-157;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'lab host="E. coli DH10B cells"
                                                                                                                                                                                                                                                                                                                                                                      1. .736
/organism="Picea glauca"
/mol_type="mRNA"
/strain="pg-653"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:3330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="GQ0085_M24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 72.7%;
al Similarity 94.8%;
565; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                 source
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                                                                    /organism="picea glauca"
/mol_type="mRNA"
/strain="pg-653"
/db xref="taxon:330"
/clone="GQ0165_M24"
/sex="Hexmaphrodite"
/tissue_type="Xylem, pith, cambium, phloem, bark"
/dev_etage="Eximary & secondary shoot, secondary phloem
pooled from plants fertilized with low and high NH4NO3"
/lab_host="E. coli DH10B cells"
/clone_lib="GQ016: Primary, secondary SHOOT -N fertil.
Treatments"
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                                                                                                                                                                                                                                                                                                                           (+) XR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                                                                                                   /note="Organ: Main stem region producing secondary gro
on 60 cm tall seedlings; Vector: pBluescript II SK (+)
Site 1: ECO-RI; Site 2: Xho-I; CDNA was prepared from
of poly A+ selected RNA and was directionally ligated
the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (In
vitrogen) for propagation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 CCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 GICACTICAICAAAAGGACAGIAGAAAAGGAAGGIGGCACCIACAAAIGCCAICAIIGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 ATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CACCCACGAGGAGCATCGTGGAAAAAGAAGAAGATCTCCAACCACGTCTTCAAAGAAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 ATTGATGTGATTG---CAGTGAGACTTTTCAACAAGGGTAATATCGGGAAACCTCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 ATTGATGTGATGGTCCGATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602 CCACGICITCAAAGCAAGIGGAIIGAIGIGAIAITCICCACIGACGIAAGGGAIGACGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         610;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 480.8; DB 7;
Pred. No. 9e-140;
0; Mismatches 32;
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Plate: 5 row: 24 column: M
Seq primer: T7 Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 93.6%;
Matches 510; Conservative
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Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MNS268594 Clone ID:
GQ0165_M24 Clones available Through: John MacKay, Ph. D. Professeur
adjoint Assistant professor EMAIL: jmackayorsvs.ulaval.ca Centre
de Recherche en Biologie Porestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA GIK 7P4
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GQ0165.B7 M24 GQ016: Primary, secondary SHOOT -N fertil. Treatments
Picea glauca cDNA clone GQ0165_M24 3', mRNA sequence.
CO481168
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Picea.

1 (bases 1 to 610)
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Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA GIK 7P4
Fax: 418 656 1493
Email: jmackay@rsvs.ulaval.ca
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Arborea EST sequencing in Picea glauca (white spruce) Unpublished (2004)
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/tissue_type="Protoplasts" /
/tissue_type="Protoplasts" /
/lab host="E. coli DH10B" /
/clone lib="Cuol Rice Blast BAC Library" /
/note="Vector: pBACWICH; Site_1: HindII; Site_2: HindIII; /
/note="Vector: pBACWICH; Site_1: HindIII; /
/note="Vector: pBACWICH; Site_1: Jack-indiving numerous aspects of the fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater
mgxb0003F18f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0003F18f, genomic survey sequence.
AQ362115.1 GI:4211034
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Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 839)
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larity 99.4%; Pred. No. 4.1e-99;
Conservative 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 58
High quality sequence stop: 454.
                                                                                                                 Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
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Contact: Dean RA
Clemson University Genomics Institute
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/strain="70-15"
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CG206846 158 654 bp DNA linear GSS 21-AUG-2003 TOS0467 TAMU Rice Japonica Nipponbare BAC Library (Hind III) Oryza sativa (japonica cultivar-group) genomic clone TOSJNBh019I10h,
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erhartoideae; Oryzae; Oryza.

1. (bases 1 to 654)
Li, Y. Wu, C., Santos, T., Uhm, T., Liu, D. and Zhang, H.-B.
BAC end sequences to close the gaps of a rice physical map at TAMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="TAMU Rice Japonica Nipponbare BAC Library (Hind III)"
  733
                                      517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/do xref="taxon:39947"
/clone="TOSJNBh019110h"
                      679 CAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGGACGACACGCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Texas A & M University
TAMU 2474, College Station, TX 77843-2474, USA
THI: 979 862 4800
Fax: 979 862 4790
Email: c-vwloheo.tamu.edu
Seg primer: M13 universal Forward GTAAAACGACGGCCAGT
Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab host="E. coli DH10B"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="leaf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics and Biotechnology
                                                                                                                                                                                 genomic survey sequence.
                                                                                                                                                                                                                                  CG206846.1 GI:34097907
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CG206846/c
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/done lib="1550 - RescueMu Grid M"
//lone lib="1550 - RescueMu Grid M"
//note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi, Site 2: BglII;
RescueMu is a 4.9 kb; modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.ramb.iastae.edu' and follow the links for
'RescueMu.' Grid M was grown at University of Arizona in
2001. DNA was extracted from leaf punches, double digested
using BamHi and BglII, and ligated to form circular
plasmids. DH10B cells were transformed and then screened
                                                                                                                                                                                                                                                                                              GSS 17-DEC-2002
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    CCCCCACCACGAGGAGCATCGTGGAAAAAAAAGAAGTTCCAACCACCTCTCAAAGCAA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                        151 GTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCATTGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      619 GTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was trimmed. Post-ligation
                                                                                                                                                                         CAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGACACGCTGAA 37
                                                                                                                                                                                                                                                                             3590_1 83_1 F06.y_1 3590 - RescueMu Grid M Zea mays genomic, genomic survey sequence.
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/cultivar="mixed background W23/A188/B73/K55"
/db xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
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Plate: 3590_1_83_1 column: 11
Class: transposon-tagged.
Location/Qualifiers
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Department of Biological Sciences
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       walbot@stanford.edu
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BZ591291.1 GI:27226352
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on LB plate
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Matches 341; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             559 CCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA 618
                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Beparnatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. (bases 1 to 496)
ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Biological Sciences Stanford University 55 California Ave, Palo Alto, CA 94304, USA 55 California Ave, Palo Alto, CA 94304, USA 55 California Ave, Palo Alto, CA 94304, USA 57 25 8221 Eax: 650 725 8221 Email: walbot@stanford.edu possible ligation site so sequence was trimmed. Post-ligation plate: 119119 row: 18
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/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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Best Local Similarity 96.3%;
Matches 342; Conservative
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                                                                                                                                                      survey sequence. CG730119
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/ taw_wose==uniou=
/clone lib==ulil8 - RescueMu Grid S"
/note=="Organ: leaf; Vector: RescueMu (engineered from
/note=="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamH1; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
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Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
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                                                                                                                                                                                                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bupermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD Clade: Panicoideae, Andropogoneae; Zea.
1 (bases 1 to 469)
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Very probable ligation site found so sequence was trimmed.

Post-ligation sequence submitted separately.

Plate: 1118056 row: 40
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/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db xref="taxon:4577"
/fissue_type="laaf"
/dev stage="adult"
/lab_host="DH10B"
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Tel: 650 723 2227
Fax: 650 725 8221
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